



#3

1

## SEQUENCE LISTING

&lt;110&gt; Reiter, Yoram

&lt;120&gt; SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES

&lt;130&gt; 02/23339

&lt;160&gt; 20

&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; synthetic peptide

&lt;400&gt; 1

Ile Met Asp Gln Val Pro Phe Ser Val  
1 5

&lt;210&gt; 2

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; synthetic peptide

&lt;400&gt; 2

Tyr Leu Glu Pro Gly Pro Val Thr Val  
1 5

&lt;210&gt; 3

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; synthetic peptide

&lt;400&gt; 3

Leu Leu Phe Gly Tyr Pro Val Tyr Val  
1 5

&lt;210&gt; 4

a1

<211> 1048

<212> DNA

<213> Homo sapiens

<400> 4  
 atgatccagc gtactccaaa gattcagggt tactcacgtc atccagcaga gaatggaaaag 60  
 tcaaatttcc tgaattgcta tgtgtctggg ttcatccat ccgacattga agttgactta 120  
 ctgaagaatg gagagagaat tgaaaaagt gagcattcag acttgtcttt cagcaaggac 180  
 tggctcttct atctcttgta ttatactgag ttcaccccca ctgaaaaaga tgagtatgcc 240  
 tgccgtgtga accacgtgac tttgtcacag cccaagatag ttaagtggga tcgagacatg 300  
 ggtggcgggt gaagcggcgg tggaggctct ggtggagggt gcagcggctc tcaactccatg 360  
 aggtatttct tcacatccgt gtcccgcccc gcccggggg agccccgctt catcgcatg 420  
 ggctacgtgg acgacacgca gttcgtgcgg ttcgacagcg acgccgcgag ccagaggatg 480  
 gagccgcggg cgccgtggat agagcaggag ggtccggagt attgggacgg ggagacacgg 540  
 aaagtgaagg ccactcaca gactcaccga gtggacctgg ggacctgcg cggctactac 600  
 aaccagagcg aggccggttc tcacaccgtc cagaggatgt atggctgcga cgtgggggtcg 660  
 gactggcgct tcctccgcgg gtaccaccag tacgcctacg acggcaagga ttacatcgcc 720  
 ctgaaagagg acctgcgtc ttggaccgcg gcggacatgg cagctcagac caccaagcac 780  
 aagtgggagg cgccccatgt ggcggagcag ttgagagcct acctggaggg cactgctgtg 840  
 gagtggctcc gcagatacct ggagaacggg aaggagacgc tgcagcgcac ggacgcccc 900  
 aaaacgcaca tgactcacca cgctgtctct gaccatgaag ccaccctgag gtgctggggc 960  
 ctgagcttct accctgcgga gatcacactg acctggcagc ggacttgag gaatctttga 1020  
 ggcaatgaag atggagctgc gggactga 1048

<210> 5

<211> 415

<212> PRT

<213> Artificial

<220>

<223> human beta2 microglobulin linked to MHC class I heavy chain

<400> 5

Met Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala  
 1 5 10 15  
 Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His  
 20 25 30  
 Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu  
 35 40 45  
 Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr  
 50 55 60

Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala  
 65 70 75 80  
 Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp  
 85 90 95  
 Asp Arg Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
 100 105 110  
 Gly Gly Ser Gly Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser  
 115 120 125  
 Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp  
 130 135 140  
 Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met  
 145 150 155 160  
 Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp  
 165 170 175  
 Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln Thr His Arg Val Asp  
 180 185 190  
 Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His  
 195 200 205  
 Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe  
 210 215 220  
 Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala  
 225 230 235 240  
 Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln  
 245 250 255  
 Thr Thr Lys His Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg  
 260 265 270  
 Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu  
 275 280 285  
 Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met  
 290 295 300  
 Thr His His Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala  
 305 310 315 320  
 Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly  
 325 330 335  
 Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly  
 340 345 350  
 Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln  
 355 360 365  
 Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro  
 370 375 380  
 Leu Thr Leu Arg Trp Glu Gln Ser Thr Arg Gly Gly Ala Ser Gly Gly  
 385 390 395 400  
 Gly Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp  
 405 410 415

&lt;210&gt; 6

&lt;211&gt; 280

&lt;212&gt; PRT

<213> Homo sapiens

<400> 6

Gly Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro Gly  
1 5 10 15  
Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln  
20 25 30  
Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro Arg  
35 40 45  
Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp Gly Glu Thr  
50 55 60  
Arg Lys Val Lys Ala His Ser Gln Thr His Arg Val Asp Leu Gly Thr  
65 70 75 80  
Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Val Gln  
85 90 95  
Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu Arg Gly  
100 105 110  
Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Lys Glu  
115 120 125  
Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Thr Thr Lys  
130 135 140  
His Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg Ala Tyr Leu  
145 150 155 160  
Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys  
165 170 175  
Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met Thr His His  
180 185 190  
Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser Phe  
195 200 205  
Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln  
210 215 220  
Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr  
225 230 235 240  
Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln Arg  
245 250 255  
Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu  
260 265 270  
Arg Trp Glu Gln Ser Thr Arg Gly  
275 280

<210> 7

<211> 100

<212> PRT

<213> Homo sapiens

<400> 7

Met Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala  
 1 5 10 15  
 Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His  
 20 25 30  
 Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu  
 35 40 45  
 Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr  
 50 55 60  
 Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala  
 65 70 75 80  
 Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp  
 85 90 95  
 Asp Arg Asp Met  
 100

<210> 8

<211> 36

<212> DNA

<213> Artificial

<220>

<223> synthetic oligonucleotide

<400> 8

aggagatata catatgggct ctcaactccat gaggta

36

<210> 9

<211> 43

<212> DNA

<213> Artificial

<220>

<223> synthetic oligonucleotide

<400> 9

cgggctttgt tagcaccgat tcataggtga ggggcttggg caa

43

<210> 10

<211> 15

<212> PRT

<213> Artificial

<220>

<223> linker peptide

<400> 10

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 1 5 10 15

<210> 11

<211> 35

<212> DNA

<213> Artificial

<220>

<223> synthetic oligonucleotide

<400> 11

ggagatatac atatgatcca gcgtactcca aagat

35

<210> 12

<211> 49

<212> DNA

<213> Artificial

<220>

<223> synthetic oligonucleotide

<400> 12

cgggctttgt tagcagccga attcattaca tgtctcgatc ccacttaac

49

<210> 13

<211> 41

<212> DNA

<213> Artificial

<220>

<223> synthetic oligonucleotide

<400> 13

ggaaggcgtt ggcgcatatg atccagcgta ctccaaagat t

41

<210> 14

<211> 50

<212> DNA

<213> Artificial

<220>

<223> synthetic oligonucleotide

<400> 14

ggaagcggcg gtggaggctc tggaggaggt ggcagcggct ctactccat

50

<210> 15

<211> 50

<212> DNA

<213> Artificial

<220>

<223> synthetic oligonucleotide

<400> 15

ggaagcggcg gtggaggctc tggaggaggt ggcagcggct ctcactccat

50

<210> 16

<211> 43

<212> DNA

<213> Artificial

<220>

<223> synthetic oligonucleotide

<400> 16

gggagaattc ttactcccat ctcagggtga ggggcttggg caa

43

<210> 17

<211> 14

<212> PRT

<213> Artificial

<220>

<223> specific biotinylation peptide sequence

<400> 17

Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp  
1 5 10

<210> 18

<211> 11

<212> PRT

<213> Artificial

<220>

<223> linker

<400> 18

Gln Ser Thr Arg Gly Gly Ala Ser Gly Gly Gly  
1 5 10

<210> 19

<211> 100

<212> DNA

<213> Artificial

<220>

<223> synthetic oligonucleotide

<400> 19

cagtaaaagc tttttatcag cctccgaact gtggatgcct ccacgccgaa cctccaccag 60

aaccacctcc ggacccgccca cctccctccc atctcagggt 100

<210> 20

<211> 39

<212> DNA

<213> Artificial

<220>

<223> BirA recognition tag sequence

<400> 20

ggaatctttg aggcaatgaa gatggagctg cgggactga 39

a!

